

10 30 50
 GTGAGATGGTGGCTTTTCATGAATTCCCCCAAGAGCCAAGCTCTCCATCTAGTGGACAG
 70 90 110
 GGAAGCTAGCAGCAAACCTTCCCTTCACTACGAACTTCATTGCTTGGCCCAAAAGAGAG
 130 150 170
 TTAATTCAATGTAGACATCTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTT
 190 210 230
 GCATTTCATGGAGGGCAACTAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTA
 250 270 290
 TGCACAGGGTGAACAAGATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTAT
 M D Y Q V S S P I Y D I N Y
 310 330 350
 TATACATCGGAGCCCCTGCCCCAAAATCAATGTGAAGCAAATCGCAGCCCCGCCTCCTGCCT
 Y T S E P C P K I N V K Q I A A R L L P
 370 390 410
 CCGCTCTACTCACTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCATCCTCATC
 P L Y S L V F I F G F V G N M L V I L I
 430 450 470
 CTGATAAACTGCCAAAGGCTGGAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATC
 L I N C Q R L E S M T D I Y L L N L A I
 490 510 530
 TCTGACCTGTTTTTCTTCTTACTGTCCCTTCTGGGCTCACTATGCTGCCGCCAGTGG
 S D L F F L L T V P F W A H Y A A A Q W
 550 570 590
 GACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCT
 D F G N T M C Q L L T G L Y F I G F F S
 610 630 650
 GGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTATCGTCCATGCTGTG
 G I F F I I L L T I D R Y L A I V H A V
 670 690 710
 TTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTG
 F A L K A R T V T F G V V T S V I T W V
 730 750 770
 GTGGCTGTGTTTGGCTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTT
 V A V F A S L P G I I F T R S Q K E G L
 790 810 830
 CATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAG
 H Y T C S S H F P Y S Q Y Q F W K N F Q
 850 870 890
 ACATTAAAGATAGTCATCTTGGGGCTGGTCTGCCGCTGCTTGTCTATGGTCATCTGCTAC
 T L K I V I L G L V L P L L V M V I C Y
 910 930 950
 TCGGGAATCTCAAAAACCTCTGCTTCGGTGTGCAAAATGAGAAGAAGAGGCACAGGGCTGTG
 S G I L K T L L R C R N E K K R H R A V
 970 990 1010
 AGGCTTATCTTACCATCATGATTGTTTATTTTCTTCTTCTGGGCTCCCTACAACATTGTC
 R L I F T I M I V Y F L F W A P Y N I V
 1030 1050 1070
 CTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGG
 L L L N T F Q E F F G L N N C S S S N R
 1090 1110 1130
 TTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCC
 L D Q A M Q V T E T L G M T H C C I N P
 1150 1170 1190
 ATCATCTATGCCTTTTGTGCGGGAGAGTTTCAGAACTACCTCTTAGTCTTCTTCAAAAG
 I I Y A F V G E K F R N Y L L V F F Q K
 1210 1230 1250
 CACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCGAGCGA
 H I A K R F C K C C S I F Q Q E A P E R
 1270 1290 1310
 GCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGTGACAC
 A S S V Y T R S T G E Q E I S V G L *
 1330 1350 1370
 GGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTTTTTCATACACA

FIGURE 1A

1390 1410
GCCTGGGCTGGGGGTGGGGTGGAAGAGGTCTTTT

10067500-020000

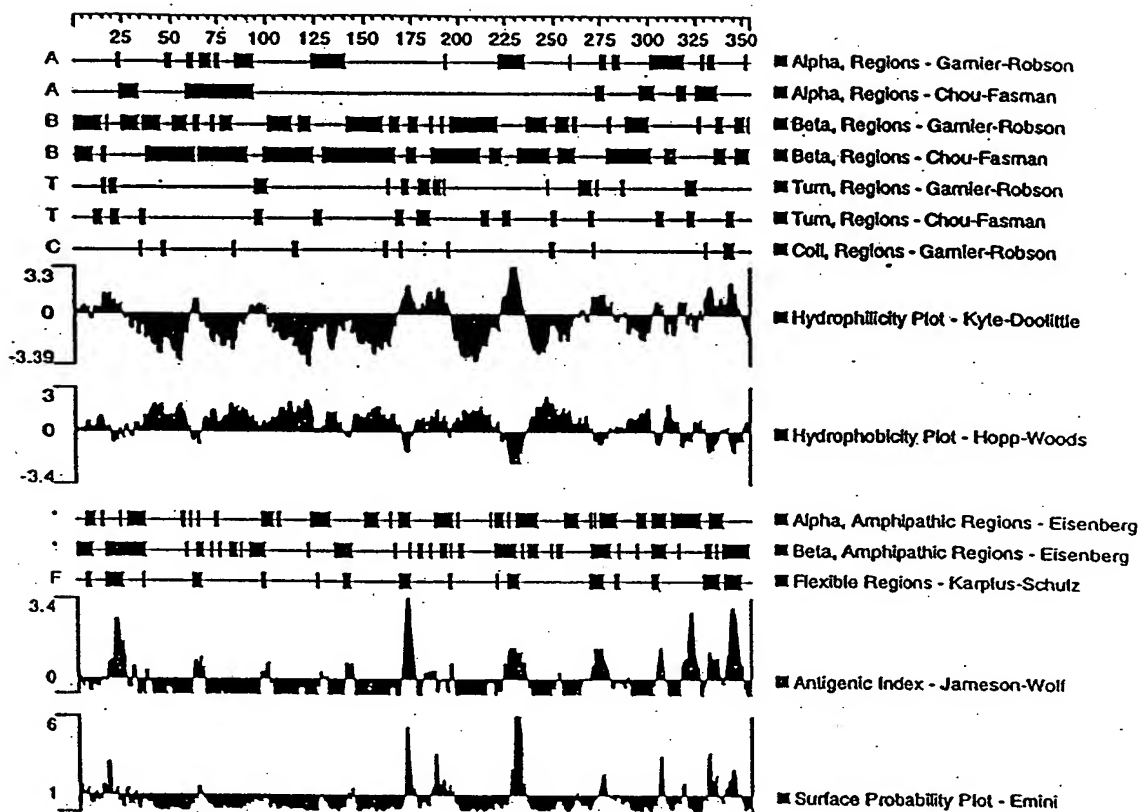
FIGURE 1B

[illegible]

4	QVSSPIYDINYYTSEPCPKINVKQIAARLLPPLYSLVFIFGFVGNMLVIL	53
18	EEVTTFDDYDY..GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVL	65
54	ILINCQRLESMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQL	103
66	ILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKL	115
104	LTGLYFIGFFSGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITW	153
116	FTGLYHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITW	165
154	VVAVFASLPGIIFTRSQKEGLHYTCSSHPYSQYQFWKNFOTLKIVILGL	203
166	LVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG...WNNFHTIMRNILGL	211
204	VLPLLVMVICYSGILKTLLRCRNEKKRHRVRLIFTIMIVYFLFWAPYNI	253
212	VLPLLIMVICYSGILKTLLRCRNEKKRHRVRVIFTIMIVYFLFWTPYNI	261
254	VLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEK	303
262	VILLNTFQEFFGLSNCESTSOLDQATQVTETLGMTHCCINPIIYAFVGEK	311
304	FRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRS...TGEQEISV	350
312	FRSLFHIALGCRIA.PLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
351	G 351	
361	G 361	

FIGURE 2

Figure 3



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Anti-CCR 5 1D8 VH Sequence

1 CAGGTGCAGCTGCAGGAGTCGGGCCCAAGGACTGGTG AAGCCTTGGAGACCCCTGTCCCTC
1 Q V Q L Q E S G P G L V K P S E T L S L
61 ACCTGCACTGTCCTCTGGTGGCTCCATCAGTAGTTCTACTGGAGCTGGATCOGGCAGCCC
21 T C T V S G G S I S S F Y W S W I R Q P
121 GCCGGGAAGGGA CTGGACTGGATTGGGCGTATCTATACCAGCGGGAACACCAACTACAAC
41 A G K G L D W I G R I Y T S G N T N Y N
181 CCTCCCAAGAGT CGAGTCAACATGTCAGTAGACACGTCCAAGAACCGGTTCCTCCCTG
61 P S L K S R V T M S V D T S K N R F S L
241 AAAC TGAGCTCTGTGACCGCCGGGACACGGCCGCTATTACTGTGGAGAGATCGGGGGC
81 K L S S V T A A D T A V Y Y C A R D R G
301 AGCAGCTGGTACCCGATGCTTTTGATATCTGGGGCCAAAGGACAATGGTCAACCTCTCC
101 S S W Y P D A F D I W G Q G T M V T V S
361 TCA
121 S

Anti-CCR 5 1D8 VK Sequence

1 GATATTGTGTGACGCATCTCCAGGCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACC
1 D I V L T H S P G T L S L S P G E R A T
61 CTCCTCTGCAGGGCCAGTCAGCGTGTACACGACGCTGCTTACCTGGTACCAGCAGAAA
21 L S C R A S Q R V T S S C L A W Y Q Q K
121 OCTGGCCAGGCTCCAGGCTCTCATCTATGGTACATCCAGCAGGGGCCACTGGCATCCCA
41 P G Q A P R L L I Y G T S S R A T G I P
181 GACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCAACATCAGCAGACTGGAG
61 D R F S G S G S G T D F T L T I S R L E
241 OCTGAAGATTTTGAGTGTATTACTGTGAGCAGTATGTTAGCTCAOCTCTCACTTCGGC
81 P E D F A V Y Y C Q Q Y V S S P L T F G
301 CAAGGGACACGACTCGAGATCAAAAGT
101 Q G T R L E I K R

Anti - CCR5 3C9 VH

1 GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTA AAG TCT GGG GGG TCC CTT AGA CTC 60
1 E V Q L V E S G G G L V K S G G S L R L 20

CDR1

61 TCC TGT GCA GCC TCC GGA TTC ACT TTC AGT AAC GCC TGG ATG ACC TGG GTC CGC CAG GCT 120
21 S C A A S G F T F S N A W M T W V R Q A 40

CDR2

121 CCA GGG AAG AGG CTG GAG TGG GTT GGC CGT ATT AAA AGC AAT GCT GAT GGT GGG TCA ACA 180
41 P G K R L E W V G R I K S N A D G G S T 60

181 GAC TAC GCT GCA CCC GTG AAA GGC AGA TTC ACC ATC TCA AGA GAT GAT TCA AAA AAC ACG 240
61 D Y A A P V K G R F T I S R D D S K N T 80

241 CTG TAT CTG CAA ATG AAC AGC CTG AAA ACC GAG GAC ACA GCC GTG TAT TAC TGT AAC ACA 300
81 L Y L Q M N S L K T E D T A V Y Y C N T 100

CDR3

301 GAT AAG GGT GGG AGC TAC CCC TAC TAC TAC TAC GGT ATG GAC GTC TGG GGC CAA GGG ACC 360
101 D K G G S Y P Y Y Y Y G M D V W G Q G T 120

361 ACG GTC ACC GTC TCC TCA G 379
121 T V T V S S 127

Anti-CCR5 3C9 VK

1 GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC 60
1 D I Q M T Q S P S S L S A S V G D R V T 20

CDR1

61 ATC ACT TGC CGG GCA AGT CAG GGC ATT AGA AAT GAT TTA GGC TGG TAT CAG CAG AAA CCA 120
21 I T C R A S Q G I R N D L G W Y Q Q K P 40

CDR2

121 GGG AAA GCC CCT AAG CGC CTG ATC TAT GAT GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA 180
41 G K A P K R L I Y D A S S L Q S G V P S 60

181 AGG TTC AGC GGC AGT GGA TCT GGG ACA GAA TTC ACT CTC ACA ATC AGC AGC CTG CAG CCT 240
61 R F S G S G S G T E F T L T I S S L Q P 80

CDR3

241 GAA GAT TTT GCA ACT TAT TAC TGT CTA CAG CAT AAT AGT TAC CCA TTC ACT TTC GGC CCT 300
81 E D F A T Y Y C L Q H N S Y P F T F G P 100

301 GGG ACC AAA GTG GAT ATC AAA CGA 324
101 G T K V D I K R 108

Fig. 5

Anti -CCR5 9E6 VH

1 GAG GTG CAG CTG GTG GAG TCT GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC 60
1 E V Q L V E S G P G L V K P S E T L S L 20

CDR1

61 ACC TGC ACT GTC TCT GGT GGC TCC ATC AGT AGT TAC TAC TGG AGC TGG ATC CGG CAG CCC 120
21 T C T V S G G S I S S Y Y W S W I R Q P 40

CDR2

121 CCA GGG AAG GGA CTG GAG TGG ATT GGG TAT ATC TAT TAC AGT GGG AGC ACC AAC TAC AAC 180
41 P G K G L E W I G Y I Y Y S G S T N Y N 60

181 CCC TCC CTC AAG AGT CGA GTC ACC ATA TCA GTA GAC ACG TCC AAG AAC CAG TTC TCC CTG 240
61 P S L K S R V T I S V D T S K N Q F S L 80

241 AAG CTG AGC TCT GTG ACC GCT GCG GAC ACG GCC GTG TAT TAC TGT GCG AGA GAT GTC ATG 300
81 K L S S V T A A D T A V Y Y C A R D V M 100

CDR3

301 CAG CAG CCG GTA CCG GGT TAC TAC TAC TAC TAC GGT ATG GAC GTC TGG GGC CAA GGA ACC 360
101 Q Q P V R G Y Y Y Y Y G M D V W G Q G T 120

361 CTG GTC ACC GTC TCC TCA 378

121 L V T V S S 126

Anti -CCR5 9E6 VK

1 GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTG TCT TTG TCT CCA GGG GAA AGA GTC ACC 60
1 E I V L T Q S P G T L S L S P G E R V T 20

CDR1

61 CTC TCC TGC AGG GCC AGT CAG AGA GTT AGC AAC AGC TAC TTA GCC TGG TAC CAG CAG AAA 120
21 L S C R A S Q R V S N S Y L A W Y Q Q K 40

CDR2

121 CCT GGC CAG GCT CCC AGG TTC CTC ATC TAT GGT GTA TCC AGC AGG GCC ACT GGC ATC CCA 180
41 P G Q A P R F L I Y G V S S R A T G I P 60

181 GAC AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGA CTG GAG 240
61 D R F S G S G S G T D F T L T I S R L E 80

CDR3

241 CCT GAA GAT TTT GCA GTG TAT TAC TGT CAG CAG TAT GGT AGT TCA CCG TGG ACG TTC GGC 300
81 P E D F A V Y Y C Q Q Y G S S P W T F G 100

301 CAA GGG ACC AAG GTG GAA ATC AAA CGA 327
101 Q G T K V E I K R 109

Fig. 6